AMENDMENTS

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (currently amended) A method for detecting different mRNAs in a sample comprising:

hybridizing the sample with a microarray substrate, wherein the substrate has a plurality of different immobilized probes and wherein the probes are suitable for multiple bases primer extension reactions;

synthesizing primer extension products with a nucleic acid polymerase, appropriate reagents and conditions, from the primers and using the mRNAs as templates wherein the primer extension products comprise 5' regions of the mRNAs; and

detecting the primer extension products to determine the level of said different mRNAs wherein target regions of the probes are distributed along the mRNAs ~~substantially entire mRNA transcript sequences are detected~~.

2. (original) The method of Claim 1 wherein the nucleic acid polymerase is a reverse transcriptase.

3. (original) The method of Claim 2 wherein the reverse transcriptase is a thermostable reverse transcriptase.

4. (original) The method of Claim 2 wherein the probes are oligonucleotide probes.

5. (original) The method of Claim 4 wherein the oligonucleotide probes are immobilized on the substrate in 5'-3' direction.

6. (previously amended) The method of Claim 5 wherein the oligonucleotide probes are synthesized on the substrate in 5'-3' direction.

7. (previously amended) The method of Claim 6 wherein said different RNAs comprise at least 50 RNAs.

8. (previously amended) The method of Claim 7 wherein said different RNAs comprise at least 100 RNAs.

9. (previously amended) The method of Claim 8 wherein said different RNAs comprise at least 1000 RNAs.

10. (previously amended) The method of Claim 9 wherein said different RNAs comprise at least 5000 RNAs.

11. (original) The method of Claim 8 wherein each of the RNAs is targeted by at least 2 probes.

12. (original) The method of Claim 11 wherein each of the RNAs is targeted by at least 5 probes.

13. (original) The method of Claim 12 wherein each of the RNAs is targeted by at least 10 probes.

14. (original) The method of Claim 13 wherein each of the RNAs is targeted by at least 20 probes.

15. (original) The method of Claim 11 wherein the plurality of probes have at least 100 probes per cm^2 of the substrate.

16. (original) The method of Claim 15 wherein the plurality of probes have at least 1000 probes per cm^2 of the substrate.

17. (original) The method of Claim 16 wherein the plurality of probes have at least 10000 probes per cm^2 of the substrate

18. (original) The method of Claim 11 wherein the extension products are detected by using a label.

19. (original) The method of Claim 18 wherein the label is incorporated during the synthesizing.

20. (previously amended) The method of Claim 18 wherein the label is attached to the extension products after the synthesizing of primer extension products with a nucleic acid polymerase.

21. (canceled)

22. (canceled)

23. (canceled)

24. (previously amended) The method of Claim 19 wherein the reagent comprises at least one type of dNTP.

25. (original) The method of Claim 24 wherein the reagent comprises dATP, dCTP, dGTP, and dTTP.

26. (previously amended) The method of Claim 11 wherein the probes comprise tiling probes that are selected to tile regions of the RNA, and wherein sequence variations are determined by detecting the extension products of the tiling probes.

27. (original) The method of Claim 26 wherein the sequence variations are SNPs.

28. (previously amended) The method of Claim 11 wherein the probes comprise tiling probes that are selected to tile the bordering regions of exons or putative exons, and wherein the arrangement of exons in the RNAs is determined by detecting the extension products of the tiling probes.

29. (previously amended) The method of Claim 11 wherein the probes comprise probes that are designed to target subregions of a genomic sequence and whether the subregions of the genomic sequence are transcribed is determined by detecting the extension products of the probes designed to target the subregions of the genomic sequence.

30. (previously presented) The method of Claim 1 wherein the sample is fragmented to generate said different RNAs from a single target RNA.